



IFWO

RAW SEQUENCE LISTING

DATE: 03/08/2004

PATENT APPLICATION: US/10/781,102

TIME: 15:02:18

Input Set : A:\PC10350B SEQ LIST.ST25.txt

Output Set: N:\CRF4\03082004\J781102.raw

3 <110> APPLICANT: Pfizer Inc.
 4 Fidock, Mark D.
 6 <120> TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
 8 <130> FILE REFERENCE: PC10350B
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/781,102
 C--> 10 <141> CURRENT FILING DATE: 2004-02-18
 10 <150> PRIOR APPLICATION NUMBER: US 60/177,326
 11 <151> PRIOR FILING DATE: 2000-01-20
 13 <150> PRIOR APPLICATION NUMBER: US 09/663,481
 14 <151> PRIOR FILING DATE: 2000-09-15
 16 <150> PRIOR APPLICATION NUMBER: UK 9922125.1
 17 <151> PRIOR FILING DATE: 1999-09-17
 19 <160> NUMBER OF SEQ ID NOS: 21
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 516
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
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 34 Leu Arg Leu Arg Tyr Met Val Lys Gln Leu Glu Asn Gly Glu Ile Asn
 35 20 25 30
 38 Ile Glu Glu Leu Lys Lys Asn Leu Glu Tyr Thr Ala Ser Leu Leu Glu
 39 35 40 45
 42 Ala Val Tyr Ile Asp Glu Thr Arg Gln Ile Leu Asp Thr Glu Asp Glu
 43 50 55 60
 46 Leu Gln Glu Leu Arg Ser Asp Ala Val Pro Ser Glu Val Arg Asp Trp
 47 65 70 75 80
 50 Leu Ala Ser Thr Phe Thr Gln Gln Ala Arg Ala Lys Gly Arg Arg Ala
 51 85 90 95
 54 Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala Val Gln Ala Gly
 55 100 105 110
 58 Ile Phe Val Glu Arg Met Phe Arg Arg Thr Tyr Thr Ser Val Gly Pro
 59 115 120 125
 62 Thr Tyr Ser Thr Ala Val Leu Asn Cys Leu Lys Asn Leu Asp Leu Trp
 63 130 135 140
 66 Cys Phe Asp Val Phe Ser Leu Asn Gln Ala Ala Asp Asp His Ala Leu
 67 145 150 155 160
 70 Arg Thr Ile Val Phe Glu Leu Leu Thr Arg His Asn Leu Ile Ser Arg
 71 165 170 175
 74 Phe Lys Ile Pro Thr Val Phe Leu Met Ser Phe Leu Asp Ala Leu Glu
 75 180 185 190

ENTERED

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79      195      200      205
82 Ala Asp Val Thr Gln Thr Val His Cys Phe Leu Leu Arg Thr Gly Met
83      210      215      220
86 Val His Cys Leu Ser Glu Ile Glu Leu Leu Ala Ile Ile Phe Ala Ala
87 225      230      235      240
90 Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn Ser Phe His Ile
91      245      250      255
94 Gln Thr Lys Ser Glu Cys Ala Ile Val Tyr Asn Asp Arg Ser Val Leu
95      260      265      270
98 Glu Asn His His Ile Ser Ser Val Phe Arg Leu Met Gln Asp Asp Glu
99      275      280      285
102 Met Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe Val Glu Leu Arg
103      290      295      300
106 Ala Leu Val Ile Glu Met Val Leu Ala Thr Asp Met Ser Cys His Phe
107 305      310      315      320
110 Gln Gln Val Lys Thr Met Lys Thr Ala Leu Gln Gln Leu Glu Arg Ile
111      325      330      335
114 Asp Lys Pro Lys Ala Leu Ser Leu Leu Leu His Ala Ala Asp Ile Ser
115      340      345      350
118 His Pro Thr Lys Gln Trp Leu Val His Ser Arg Trp Thr Lys Ala Leu
119      355      360      365
122 Met Glu Glu Phe Phe Arg Gln Gly Asp Lys Glu Ala Glu Leu Gly Leu
123      370      375      380
126 Pro Phe Ser Pro Leu Cys Asp Arg Thr Ser Thr Leu Val Ala Gln Ser
127 385      390      395      400
130 Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe Ser Val Leu
131      405      410      415
134 Thr Asp Val Ala Glu Lys Ser Val Gln Pro Leu Ala Asp Glu Asp Ser
135      420      425      430
138 Lys Ser Lys Asn Gln Pro Ser Phe Gln Trp Arg Gln Pro Ser Leu Asp
139      435      440      445
142 Val Glu Val Gly Asp Pro Asn Pro Asp Val Val Ser Phe Arg Ser Thr
143      450      455      460
146 Trp Val Lys Arg Ile Gln Glu Asn Lys Gln Lys Trp Lys Glu Arg Ala
147 465      470      475      480
150 Ala Ser Gly Ile Thr Asn Gln Met Ser Ile Asp Glu Leu Ser Pro Cys
151      485      490      495
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155      500      505      510
158 Gly Asn Leu Asp
159      515
162 <210> SEQ ID NO: 2
163 <211> LENGTH: 3091
164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 2
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174	ctacatggtg	aagcagttgg	agaatgggga	gataaacatt	gaggagctga	agaaaaatct	240
176	ggagtacaca	gcttctctgc	tggaagccgt	ctacatagat	gagacacggc	aatcttgga	300
178	cacggaggac	gagctgcagg	agctgcggtc	agatgccgtg	ccttcggagg	tgcgggactg	360
180	gctggcctcc	accttcaccc	agcaggcccc	ggccaaaggc	cgccgagcag	aggagaagcc	420
182	caagttccga	agcattgtgc	acgctgtgca	ggctgggata	ttcgtggaac	ggatgttccg	480
184	gagaacatac	acctctgtgg	gccccactta	ctctactgcg	gttctcaact	gtctcaagaa	540
186	cctggatctc	tggtgctttg	atgtcttttc	cttgaaccag	gcagcagatg	accatgccct	600
188	gaggaccatt	gtttttgagt	tgtctgactcg	gcataacctc	atcagccgct	tcaagattcc	660
190	cactgtgttt	ttgatgagtt	tcctggatgc	cttggagaca	ggctatggga	agtacaagaa	720
192	tccttaccac	aaccagatcc	acgcagccga	tgttaccagg	acagtccatt	gcttcttgct	780
194	ccgcacaggg	atggtgcact	gcctgtcggg	gattgagctc	ctggccatca	tccttgctgc	840
196	agctatccat	gattatgagc	acacgggcac	taccaacagc	ttccacatcc	agaccaagtc	900
198	agaatgtgcc	atcgtgtaca	atgatcgttc	agtgtcggag	aatcaccaca	tcagctctgt	960
200	tttccgattg	atgcaggatg	atgagatgaa	cattttcatc	aacctcacca	aggatgagtt	1020
202	tgtagaactc	cgagccctgg	tcattgagat	gggtgttgcc	acagacatgt	cctgccattt	1080
204	ccagcaagtg	aagaccatga	agacagcctt	gcaacagctg	gagaggattg	acaagcccaa	1140
206	ggccctgtct	ctactgctcc	atgctgctga	catcagccac	ccaaccaagc	agtggttggt	1200
208	ccacagccgt	tggaccaagg	ccctcatgga	ggaattcttc	cgtcaggggtg	acaaggaggc	1260
210	agagttgggc	ctgccctttt	ctccactctg	tgaccgcact	tccactctag	tggcacagtc	1320
212	tcagataggg	ttcatcgact	tcattgtgga	gcccacattc	tctgtgctga	ctgacgtggc	1380
214	agagaagagt	gttcagcccc	tggcggatga	ggactccaag	tctaaaaacc	agcccagctt	1440
216	tcagtggcgc	cagccctctc	tggatgtgga	agtgggagac	cccaaccctg	atgtggtcag	1500
218	ctttcgttcc	acctgggtca	agcgcattca	ggagaataag	cagaaatgga	aggaacgggc	1560
220	agcaagtggc	atcaccaacc	agatgtccat	tgacgagctg	tccccctgtg	aagaagaggc	1620
222	ccccccatcc	cctgccgaag	atgaacacaa	ccagaatggg	aatctggatt	agccctgggg	1680
224	ctggcccagg	tcttcattga	gtccaaagtg	tttgatgtca	tcagcaccat	ccatcaggac	1740
226	tggctccccc	atctgtctca	agggagcgtg	gtcgtggaag	aaacaaccca	cctgaaggcc	1800
228	aaatgccaga	gatttggggg	tggggaaagg	gccccctccc	acctgacacc	cactgggggtg	1860
230	cactttaatg	ttccggcagc	aagactgggg	aacttcaggc	tccagtggtg	cactgtgcc	1920
232	atccctcagc	ctctgattc	tcttcattgg	caggtggctg	ccaggggagcg	gggagcttcc	1980
234	tggaggcttc	ccagggcctt	ggggaagggt	cagagatgcc	agccccctgg	gacctccccc	2040
236	atcctttttg	cctccaagtt	tctaagcaat	acattttggg	ggttccctca	gccccccacc	2100
238	ccagatctta	gctggcagg	ctgggtgccc	cttttctctc	cctgggaagg	gctggaatag	2160
240	gatagaaagc	tgggggtttt	cagagcccta	tgtgtgggga	ggggagtgga	ttccttcagg	2220
242	gcatggtacc	tttctaggat	ctgggaatgg	ggtggagagg	acatcctctt	cacccagaa	2280
244	ttgcgctgct	tcagccccat	ctccagcctg	atcctctgaa	tcttctctcc	ctccctttct	2340
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248	ggaccttcct	tgggactggt	ctgggcccct	ggggcttgct	gcctgccctg	agtcgggagc	2460
250	cctttgcctc	cttctctctc	cctggggctg	ggaggctcca	tccgaccaat	gtctgtaaag	2520
252	tgccttgagg	atctccccag	caaagcacct	tcagaatgta	tcgacaccag	ctgggttagg	2580
254	gtcaagggtg	cctggggagg	gtgagtaatc	ctgcattgct	aaaagagagg	gtctgtcccc	2640
256	tcctctccac	gtcccagaac	tggcccagct	gcaggcacta	agaagctcct	ccccagagac	2700
258	aagtgagggg	tagtcggtga	aaggcagatg	gacaaggggc	tcagggtctgc	tgcttctctg	2760
260	tcctctggag	agaaccagc	caggcgcggt	gcccccttct	ctcctcaggc	tcctccttgc	2820
262	ccccaccttg	ccccaggaaa	ggccaaagtc	caggtgactg	ccctccttct	ttcttgtaaa	2880
264	taccaacctg	gcatttgtac	agtgggccct	gttcatgcga	aatccacatc	catggtctcc	2940
266	tagacctgct	accttggtac	ttccacccta	ccccaccctg	agaagggcag	agacgcagtg	3000
268	gactcacccc	tgcccttggt	ttccagagcc	cctgctatag	ccagagaaca	ataaagaagg	3060

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270 gagaccagga aaaaaaaaaa aaaaaaaaaa a
273 <210> SEQ ID NO: 3
274 <211> LENGTH: 536
275 <212> TYPE: PRT
276 <213> ORGANISM: Homo sapiens
278 <400> SEQUENCE: 3
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281 1 5 10 15
284 Cys Pro Ser Pro Leu Glu Leu Lys Ser Ala Pro Ser Lys Lys Met Trp
285 20 25 30
288 Ile Lys Leu Arg Ser Leu Leu Arg Tyr Met Val Lys Gln Leu Glu Asn
289 35 40 45
292 Gly Glu Ile Asn Ile Glu Glu Leu Lys Lys Asn Leu Glu Tyr Thr Ala
293 50 55 60
296 Ser Leu Leu Glu Ala Val Tyr Ile Asp Glu Thr Arg Gln Ile Leu Asp
297 65 70 75 80
300 Thr Glu Asp Glu Leu Gln Glu Leu Arg Ser Asp Ala Val Pro Ser Glu
301 85 90 95
304 Val Arg Asp Trp Leu Ala Ser Thr Phe Thr Gln Gln Ala Arg Ala Lys
305 100 105 110
308 Gly Arg Arg Ala Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala
309 115 120 125
312 Val Gln Ala Gly Ile Phe Val Glu Arg Met Phe Arg Arg Thr Tyr Thr
313 130 135 140
316 Ser Val Gly Pro Thr Tyr Ser Thr Ala Val Leu Asn Cys Leu Lys Asn
317 145 150 155 160
320 Leu Asp Leu Trp Cys Phe Asp Val Phe Ser Leu Asn Gln Ala Ala Asp
321 165 170 175
324 Asp His Ala Leu Arg Thr Ile Val Phe Glu Leu Leu Thr Arg His Asn
325 180 185 190
328 Leu Ile Ser Arg Phe Lys Ile Pro Thr Val Phe Leu Met Ser Phe Leu
329 195 200 205
332 Asp Ala Leu Glu Thr Gly Tyr Gly Lys Tyr Lys Asn Pro Tyr His Asn
333 210 215 220
336 Gln Ile His Ala Ala Asp Val Thr Gln Thr Val His Cys Phe Leu Leu
337 225 230 235 240
340 Arg Thr Gly Met Val His Cys Leu Ser Glu Ile Glu Leu Leu Ala Ile
341 245 250 255
344 Ile Phe Ala Ala Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn
345 260 265 270
348 Ser Phe His Ile Gln Thr Lys Ser Glu Cys Ala Ile Val Tyr Asn Asp
349 275 280 285
352 Arg Ser Val Leu Glu Asn His Ile Ser Ser Val Phe Arg Leu Met
353 290 295 300
356 Gln Asp Asp Glu Met Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe
357 305 310 315 320
360 Val Glu Leu Arg Ala Leu Val Ile Glu Met Val Leu Ala Thr Asp Met
361 325 330 335
364 Ser Cys His Phe Gln Gln Val Lys Thr Met Lys Thr Ala Leu Gln Gln

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3091

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365          340          345          350
368 Leu Glu Arg Ile Asp Lys Pro Lys Ala Leu Ser Leu Leu Leu His Ala
369          355          360          365
372 Ala Asp Ile Ser His Pro Thr Lys Gln Trp Leu Val His Ser Arg Trp
373          370          375          380
376 Thr Lys Ala Leu Met Glu Glu Phe Phe Arg Gln Gly Asp Lys Glu Ala
377 385          390          395          400
380 Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp Arg Thr Ser Thr Leu
381          405          410          415
384 Val Ala Gln Ser Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr
385          420          425          430
388 Phe Ser Val Leu Thr Asp Val Ala Glu Lys Ser Val Gln Pro Leu Ala
389          435          440          445
392 Asp Glu Asp Ser Lys Ser Lys Asn Gln Pro Ser Phe Gln Trp Arg Gln
393          450          455          460
396 Pro Ser Leu Asp Val Glu Val Gly Asp Pro Asn Pro Asp Val Val Ser
397 465          470          475          480
400 Phe Arg Ser Thr Trp Val Lys Arg Ile Gln Glu Asn Lys Gln Lys Trp
401          485          490          495
404 Lys Glu Arg Ala Ala Ser Gly Ile Thr Asn Gln Met Ser Ile Asp Glu
405          500          505          510
408 Leu Ser Pro Cys Glu Glu Glu Ala Pro Pro Ser Pro Ala Glu Asp Glu
409          515          520          525
412 His Asn Gln Asn Gly Asn Leu Asp
413          530          535
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417 <211> LENGTH: 3112
418 <212> TYPE: DNA
419 <213> ORGANISM: Homo sapiens
421 <400> SEQUENCE: 4
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424 cagccgcaga ccgtggctga gcatggagct gtccccccgc agtcctccgg agatgctgga 120
426 ggagtcggat tgcccgtcac ccctggagct gaagtcagcc cccagcaaga agatgtggat 180
428 taagcttcgg tctctgctgc gctacatggt gaagcagttg gagaatgggg agataaacat 240
430 tgaggagctg aagaaaaatc tggagtagac agcttctctg ctggaagccg tctacataga 300
432 tgagacacgg caaatcttgg acacggagga cgagctgcag gagctgcggt cagatgccgt 360
434 gccttcggag gtgcgggact ggctggcctc caccttcacc cagcaggccc gggccaaagg 420
436 ccgccgagca gaggagaagc ccaagttccg aagcattgtg cacgctgtgc aggtctggat 480
438 cttcgtggaa cggatgttcc ggagaacata cacctctgtg ggccccactt actctactgc 540
440 ggttctcaac tgtctcaaga acctggatct ctggtgcttt gatgtctttt ccttgaacca 600
442 ggcagcagat gaccatgccc tgaggacat tgtttttgag ttgctgactc ggcataacct 660
444 catcagccgc ttcaagattc ccactgtgtt tttgatgagt ttcttgatg ccttgagac 720
446 aggctatggg aagtacaaga atccttacca caaccagatc cagcagccg atgttaccca 780
448 gacagtccat tgcttcttgc tccgcacagg gatggtgcac tgctgtcgg agattgagct 840
450 cctggccatc atctttgctg cagctatcca tgattatgag cacacgggca ctaccaacag 900
452 cttccacatc cagaccaagt cagaatgtgc catcgtgtac aatgatcggt cagtgtgga 960
454 gaatcaccac atcagctctg ttttccgatt gatgcaggat gatgagatga acattttcat 1020
456 caacctcacc aaggatgagt ttgtagaact ccgagccctg gtcattgaga tgggtgtggc 1080
458 cacagacatg tcctgccatt tccagcaagt gaagaccatg aagacagcct tgcaacagct 1140

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RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : A:\PC10350B SEQ LIST.ST25.txt

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:14,15,16,17,18,19,20,21

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date